

| | | 1/9 | | | |
|------|---|-----|-------------------|------|------|
| | 5'UTR | | | | |
| -29 | GGTCTTTGGTTCGTGAAGGAAGACAGC | 1+M | D L V L R K Y L L | | 10 |
| SILS | ATG GAT CTG CTG AGA AAA TAC CTT CTC | | | | 30 |
| | H V A L M G V L L A V R T T E G F R | | | | 28 |
| | CAT GTG GCT CTG ATG GGT GTT CTT CTG GCT GTA AGG ACC ACA GAA GGA CCC AGA | | | | 84 |
| | D R D W L G V S R Q L R I K A W N R | | | | 46 |
| | GAC AGG GAC CTG GGT GTC TCA AGG CAG CTC AGA ATT AAA GCA TGG AAC AGA | | | | 138 |
| | Q L Y P E W T E S Q G P D C W R G G | | | | 64 |
| | CAG CTG TAT CCA GAG TGG ACA GAA AGC CAG GGG CCT GAC TGC TGG AGA GGT GGC | | | | 192 |
| | H I S L K V S N D G P T L I G A N A | | | | 82 |
| | CAC ATA TCC CTG AAG GTT AGC AAT GAT GGG CTT ACA CTG ATT GGG GCA AAT GCT | | | | 246 |
| | S F S I A L H F P K S Q K V L P D G | | | SIL2 | 100 |
| | TCC TTC TCT ATT GCC TTG CAC TTT CCT AAA AGC CAA AAG GTG CTG CCA GAT GGG | | | | 300 |
| | Q V I W A N N T I I N G S Q V W G G | | | | 118 |
| | CAG GTC ATC TGG GCC AAC ACC ATC ATC AAT GGG AGC CAG CTG TGG GGA GGA | | | | 354 |
| | Q L V Y P Q E P D D T C I F P D G E | | | SIL1 | 136 |
| | CAG CTG GTA TAT CCC CAA GAA CCT GAT GAT ACC TGC ATC TTC CCC GAT GGG GAG | | | | 408 |
| | P C P S G P L S Q K R C F V Y V W K | | | | 154 |
| | CCC TGC CCT TCT GGT CTA TCT CAG AAA AGA TGC TTT GTT TAT GTC TGG AAG | | | | 462 |
| | T W D Q Y W Q V L G G P V S G L S I | | | | 172 |
| | ACC TGG GAC CAA TAC TGG CAA GTT CTG GGG GGC CCA GTG TCT GGA CTG AGC ATC | | | | 516 |
| | G T D K A M L G T Y N M E V T V Y H | | | | 190 |
| | GGG ACA GAC AAG GCA ATG CTG GGC ACA TAT AAC GTG AAG GTG ACT GTC TAC CAC | | | | 570 |
| | R R G S Q S Y V P L A H S S S A F T | | | | 208 |
| | CGC CGG GGG TCC CAG AGC TAT GTG CCC CTC GCT CAC TCC AGT TCA GCC TTC ACC | | | | 624 |
| | I T D Q V P F S V S V S Q L Q A L D | | | | 226 |
| | ATT ACT GAC CAG GTG CCC TTC TCT GTG AGT GTG TCT CAG CTG CAG GCT TTG GAT | | | | 678 |
| | G R N K R F L R K Q P L T F A L Q L | | | | 244 |
| | GGA AGG AAC AAG CGC TTC CTG AGA AAG CAG CCT CTG ACC TTT GCC CTC CAG CTC | | | | 732 |
| | H D P S G Y L A G A D L S Y T W D F | | | | 262 |
| | CAT GAT CCC AGT GGC TAT TTG GCT GGG GCT GAC CTT TCC TAC ACC TGG CAG TTT | | | | 786 |
| | G D S T G T L I S R A L T V T H T Y | | | | 280 |
| | GGT GAC AGT ACA GGG ACC CTG ATC TCT CGG GCA CTC ACG GTC ACT CAC ACT TAC | | | | 840 |
| | L E S G P V T A Q V V L Q A A I P L | | | | 298 |
| | CTA GAG TCT GGC CAG ACT GCA CAG GTG GTG CTG CAG GCT GCC ATT CPT CTC | | | | 894 |
| | T S C G S S P V P G T T D R H V T T | | | | 316 |
| | ACC TCC TGT GGC TCC TCT CCA GTT CCA GGC ACT ACA GAT AGG CAT GTG ACA ACT | | | | 948 |
| | A E A P G T T A G Q V P T T E V M G | | | | 334 |
| | GCA GAG GCT CCT GGA ACC ACA GCT GGC CAA GTG CCT ACT ACA GAA GTC ATG GGC | | | | 1002 |
| | T T P G Q V P T A E A P G T T V G W | | | | 352 |
| | ACC ACA CCT GGC CAG GTG CCA ACT GCA GAG GCC CCT GGC ACC ACA GTT GGG TGG | | | | 1056 |
| | V P T T E D V G T T P E Q V A T S K | | | | 370 |
| | GTG CCA ACC ACA GAG GAT GTA GGT ACC ACA CCT GAG CAG GTG GCA ACC TCC AAA | | | | 1110 |
| | V L S T T P V E M P T A K A T G R T | | | | 388 |
| | GTC TTA AGT ACA ACA CCA GTG GAG ATG CCA ACT GCA AAA GCT ACA GGT AGG ACA | | | | 1164 |

Figure 1

| | |
|---|------|
| P E V S T T E P S G T T V T Q G T T | 406 |
| CCT GAA GTG TCA ACT ACA GAG CCC TCT GGA ACC ACA GTT ACA CAG GGA ACA ACT | 1218 |
| P E L V E T T A G E V S T P E P A G | 424 |
| CCA GAG CTG GTG GAG ACC ACA GCT GGA GAG GTG TCC ACT CCT GAG CCT GCG GGT | 1272 |
| S N T S S F M P T E G T A G S L S P | 442 |
| TCA AAT ACT AGC TCA TTC ATG CCT ACA GAA GGT ACT GCA GGC TCC CTG AGT CCC | 1326 |
| L P D D T A T L V L E K R Q A P L D | 460 |
| CTG CCG GAT GAC ACT GCC ACC TTA GTC CTG GAG AAG GCG CAA GCC CCC CTG GAT | 1380 |
| C V L Y R Y G S F S L T L D I V Q G | 478 |
| TGT GTT CTG TAT CGC TAT GGC TCC TTT TCC CTC ACC CTG GAC ATT GTC CAG GGT | 1434 |
| I E S A E I L Q A V S S S E G D A F | 496 |
| ATT GAG AGT GCT GAG ATC CTA CAG GCT GTG TCA TCC AGT GAA GGA GAT GCA TTT | 1488 |
| E L T V S C Q G G L P K E A C M D I | 514 |
| GAG CTG ACT GTG TCT TGC CAA GGC GGG CTA CCC AAG GAA GCC TGC ATG GAC ATC | 1542 |
| S S P G C Q L P A Q R L C Q P V P P | 532 |
| TCA TCG CCA GGG TGT CAG CTG CCT GCC CAG CGG CTG TGT CAG CCT GTG CCC CCC | 1596 |
| S P A C Q L V L H Q V L K G G S G T | 550 |
| AGC CCA GCC TGC CAG CTG GTT TTG CAC CAG GTA CTG AAG GGT GGC TCA GGG ACC | 1650 |
| Y C L N V S L A D A N S L A M V S T | 568 |
| TAC TGC CTC AAT GTG TCT TTG GCT GAT GCC AAT AGC CTG GCG ATG GTC AGC ACC | 1704 |
| SIL3 → | |
| Q L V M P G Q E A G L R Q A P L F V | 586 |
| CAG CTT GTC ATG CCT GGG CAA GAA GCA GGC CTC AGG CAG GCT CCT CTG TTC GTG | 1758 |
| G I L L V L T A L L L A S L I Y R R | 604 |
| GGC ATC ITG CTG GTG CTA ACA GCT TTG TTG CTT GCA TCT CTG ATA TAC AGG CGA | 1812 |
| R L M K Q G S A V P L P Q L P H G R | 622 |
| AGA CTT ATG AAG CAA GGC TCA GCA GTC CCC CTT CCC CAG CTG CCA CAC GGT AGA | 1866 |
| T Q W L R L P W V F R S C P I G E S | 640 |
| ACC CAG TGG CTA CGT CTG CCC TGG GTC TTC CGC TCT TGC CCC ATT GGT GAG AGC | 1920 |
| K P L L S G Q Q V * | |
| AAA CCC CTC CTC AGT GGA CAG CAG GTC TGA GTG CTC TTA TGT GAA GTC ATG ATT | 1974 |
| SIL4 → | |
| TAC CCA GGT GGA CAG CAA GGC CTG TCT TTT CTC TGG TCT TCC CTC AGA GAC TAC | 2028 |
| SIL6 ← | |
| CAT TGC CTG AAA TAA AGA CTC AGA ACT TG | 2057 |
| SIL9 ← | |
| 3'UTR | |

Figure 1 (suite)

| | |
|--|------|
| SIL10 | |
| GTTGCTGGAAAGGAACAGACGATGGATCTGGTCTGAGAAAAATACCTTCTCCATCTGGCTCTGATGGGTGTTCTTCTGGC | 80 |
| TGTAAAGCAACAGAAAGGTGAGTGTGGAGTGTGGACATGAACAGTGTGAATTTGGGGTTGCACACCTGCTCTGTTTT | 160 |
| TCTCTCCCTAAAATGGAAGATATCAGTAGTGCTTCAGGTGCTCCACCCATTGATTAGTAGGACATGGGCAACTGA | 240 |
| GCTCCCTCCCATGATGAAGATTGGGTGCATGTGTTCAGGCACTTGGGACTGAACCTGAAACACCCCATCTACCTG | 320 |
| GATGGGTGAGAGACAGTATGTCTCCGTGGCCCTAATTTTGAATGCTCTGAATAGTGAGCTGGAACATGGGTGCCAAGG | 400 |
| TAGTAAATAGTAGTGAAACTCATTTAGGCTTTGTCTCAGGCACCTTGGGATAGGGTATTTAGGAATAGAGAAGATAGGA | 480 |
| GATAGGGAAGAGAGAAGGAGTGTGTATTGGATAGAAGGGTAATGAGGCACCTCATCCCCCTTTGGGATGGGCATG | 560 |
| GGTGAACACAGCCAGGCTTTTGTCTGGGGCTGGAAAGACAGGCAGAAAGGCTCTCAGCTGAGCATCACATGAAGGGC | 640 |
| TCTGGGGATTGGGGCTCGTGACAGGACAGGCGGGTGGGTGGGGATGGTGAGAGGCTCTGGAATGTCCCGTCTGC | 720 |
| TCTGAGGAGGAGGATTGGGAGTGGAAGAAATGGGGCATCTTATGATTCTCTGTCTTGTGGTGAGGATTCAGTGG | 800 |
| GATAATCTAGATCTCTCCCAAGAGAAATCAACAGGTTCTGTGACATGTTAGAGATGGATGAGGATAGCTGTGATG | 880 |
| TGCAGAAATATCTACATTGTACCCAGTGGCCCTTTCTCTAGATCCCTGGTCTCACAGACTTCTTGAACCTTCTCCTTG | 960 |
| ATCTGACTCTCCCTCATTCATGGTGCTATTCAAGTCTTATTCCTTTTACTATGTTGGTATTGTATTCGSAATATCTCTG | 1040 |
| TTCATATGTGTCCACCAAGGCTCTTAATATGTTGTGCTTATTTTGGATCCAGATTTTAAATCATGAAGACAT | 1120 |
| TTTATATAGTTCATGAATTTTTCATGGACTGAGTTTATATATTTTGTATTAGTGAAATTAACATTGTGTTATTTAAGA | 1200 |
| AAAAAATATTTTAAAGAAACCTACTGAATTTTGAAGGTTTTAAATTAACATGATGCTGGGATTGCTTTTGAAT | 1280 |
| GCTTCAGCCAAAAACAACGACACAAAAATAAGGATAGATAAAGCAAAATGTGACAAAATGCTAGATGTTGTGGAC | 1360 |
| CTTGGGGACACATGCGAGGCCATCAGTACCTTTTTCAGACATCTTCTTGGTCAGTTATTAATCATTTTGTATTGTCT | 1440 |
| CCCACGCCAATTTCTACTTGCCTCTAGTCCATCCTCCTCAGTGTGCCAAGTACCTCTTAAACACAAATCTGAT | 1520 |
| CATATTCAAAAAGCTTTTGAAGGTAAAGTTTATGGTATATGCCATATATCAGTACAACAAACAAATCGCTGAGGTGC | 1600 |
| CGTTGCTACAGGATAAAGTCCAACTCCTTTGCTGGCACTCCAGCCCCCACTCTATCTTCTGGCCCTCATCTCTCAT | 1680 |
| GATGTACATCAGCCACATTGCTAGTGTCTGCTCATGGCTTCTGCTCAGATGCTTTATGCCCCAGCCCACTATTACTG | 1760 |
| TCTTCTTCAGTCGACAGAGTGCAATTTACCTGTTTAAATCTATCATTTTGTATACATTGTGCAATGCTATTAATGGCT | 1840 |
| CATATTAAAGCAATGCTTGGATTATAGTAATTTATGTATATGTCTATTTTCATATCTTTAACTGAAACCCCTCAGAACC | 1920 |
| ATTTCTTTTCATTTCTTAAAGTCTTTTGACCTAGCCAGTGCTGGTACGCTGTGGTATTCAATGAGATTAATATGCAC | 2000 |
| TTTAAGGAACCTCCCTGTGTGTCATCAAGTGGCTAAGGCTCTGTGCTCCCAATGCAGGGACAGGGTTCAATCTCAGG | 2080 |
| CAGGGAACCTAGATCCCAAGGTCACAAGTTTGAAGGACCAACTACTGACCTCAGATGCCACCAACTAATCGA | 2160 |
| AGATCCCTCGTGTGCAACTAAGTCTAGTGCAGTTAAATATATTTTTTAAATGACACTTTGAATGTGAGAAATGAATGATG | 2240 |
| TGTCACAGACATGTTGTCCTCCGAGAAGGGAGTGAATGAATTTTGGGGCCCTCATAGTATATCTTCTCTTTTAGGAC | 2320 |
| CCAGAGACAGGACATGGCTGGTGTCTCAAGGAGCTCAGAAATTAAGCATGGAACAGACAGCTGTATCCAGAGTGGACA | 2400 |
| GAAGGCCAGGGGCTGACTGCTGGAGAGGTAGGAACCTTGGCAATTTCCAGGGAGGATATGTTGAAATGGGTGGGAGGG | 2480 |
| GAACGGGTTGAATGTACTTAGGAAGATAGGGAAGGAAGGNCATACAGGAGGGAAGCCAGGAGCTAATTAATGCAG | 2560 |
| CTGCCCTTTTCAGGTGGCCACATATCCTGAAGGTCAGCAATGATGGGCTACACTGATTGGGGCAAAATGCTTCTCTCTC | 2640 |
| TATTTGCTTGGCACTTCTTAAAGCCAAAGGTGCTGCCAGATGGGAGGCTCACTGGGCCAACCAACCACTCAATG | 2720 |
| GTGAGTACCTCTCGGCTCTTCCCAAGGTCAGAAATCCCTGGTATCCCAATGAGCTCAAGGAACTCTCTCTCTCTTT | 2800 |
| TTTTTTTTTTTTTACAAATATATATGTAACATATTCATGCGAGAAATTAGAAGAACACAGATTAACCAAAAAA | 2880 |

Figure 2

AAAAAATTATAGTTCGCCAATGGGGCAGAGAAGACCCAGTGGACATAGAAGTTGGATAGACTGGATTAAACTGGTT 2960
 ACCAGTATGTGACCCCTGGACAGCTCACTGAATTGTTTGTCTTCCTATCCCTTATCTATAGAATGGGGATGATACACT 3040
 TTAAGAGGTCTGTGTAGAGGATTAAATGTGATANTATATAAAGATTTTAGACAATGCTGCTGCTGTCTGTAGTA 3120
 CCTTAGTTTAGAGCCCTTGGACCCCATGGACTGTAGCCACCAGGCTCTCTGTCCATGTGGATTCTGCAGGCAAGAAT 3200
 ACTGGAGTGGGTCAACATGCACCTCCTCCAGGGGATCTTCCCACTCAGGGTTCGAACCCAGGTCTAGCTACAGATTAT 3280
 ATTGATGCTGTTATTTTACTTTTATCCCACTAGCTAGAGCACATCTCTAGACAATTTGATACATGGCTACCAATTT 3360
 GTGTCCAGTGTAGAATATACATGTGTGTCTCAGTGGCTCAGTGTGTCTGACTCTTTGCAACCCCATGGACTGTAGCC 3440
 CGGAAAGCTCCTCTGCCATGGGATTGCCAGCCAAGATACCTGAGCAGGTTGCCATTTCTCTCCAGGGGATCTTT 3520
 CAACACAGGGGATTCANTCCTTGTCTCTGTGTCTTCTGCACTGGCAGGTGTAATCTTTACCACTGAGCCACCTGGGAAC 3600
 CCGTTAGTATATACACATAAATCTTTATAGTTTCATTCTCCCTTCTACCACTCCAAATAGGTTATACCAAGGAAT 3680
 GTATTTTGGTAGCTAGGCAGTATCTCTGGAGCCCTCTCTGGGAGTCATGTTAAAGGTTTGGGTACAGTGAGGAATGC 3760
 CAGGGATTGAGGGAGATCTGTCTCTCTTTCAAGGAGCAGGCTGTGGGAGGACAGCTGGTATATCCCAAGAACCTG 3840
 ATGATACCTGCATCTTCCCGGATGGGGAGCCCTGCCCTCTGGGCCCTCTATCTCAGAAAGATGCTTTGTTATGTCTGG 3920
 AAGACCTGGGTAAGAGTTTCCCTTCTCTGGCTGTCACTCACATTAATTCATCTTCTCTACTGATCCCCCTTCTT 4000
 TGTGTCATCTCTTAAATCTGTAGATTCCCTAATCTCACTTCCCGCATGACTCTTCTCTTCCACAGCACTGACT 4080
 AACCTATATACTCTTTCTGGGAGCCCTGTCTCAATATAGTCCCATCCCATGGACCTCTCATAGGACTTTTTTTC 4160
 TGCCTACATATGACAGCTTAACTCTCTGAAATTAACCATCTTGATACATCTCTGACCTTCTCTCTGGTTCATCT 4240
 CTAACTCTGCCAGTCTCTCTTTGACAGTAACCCCTTCCCTACTCTCTTTCAGAAACCTCAGACCAATCTGGCAA 4320
 GTTCTGGGGGGCCAGTGTCTGGACTGAGCATCGGGACAGACAAGCCAATGCTGGGACATATATACATGGAAGTACTGT 4400
 CTACCCAGCCGGGGGCTCCAGAGCTATGTGCCCTCTGCTCACTCAGTTTCAGCTTCCACCTACTGGTGAAGGACTGAG 4480
 GAGGGGACAGGCCAGTTGACGGGACGGAGAAGGTGGGAGGCTGGGCTGGACAGGAAGGGGAAGAGGAATGGTGTG 4560
 TAACCTTACAGGGGACAGACCGAAGATGTGGGACAGGGATGTGGGCTTGGAGCCCTGAGGGGACAGGACGCTGG 4640
 GTTGGTGAAGAATAATGGCTGTGAAGAAGAAGCTGACAGAAAGAAGACTTATGGTTCTCACTTCTCTGACTCCAACT 4720
 CCAGACAGGTGCCCTTCTCTGTAGTGTCTCTCAGCTGCAGGCCCTTGGATGGAAGGACAGGCCCTTCTCTGAGAAACA 4800
 GCTCTGACCTTTCGCCCTCAGACTCATGATCCCATGGCTATTTGGCTGGGGCTGACCTTTCTCTACACCTGGGACTTTG 4880
 GTGACAGTACAGGACCTGATCTCTCGGCACTCAAGGTCACCTACACTTACCTACAGTGTGGCCGAGTCACTGACAG 4960
 GTGGTGTGACAGGTGCTCATCTCTCAGCTCTGTGGCTCTCTCTCAGGTCACAGGACATACAGATAGGCTGTGACAC 5040
 TGCAGAGGCTCTGGAACCAAGCTGGCCAACTGCTACTACAGAGTATGGGACACACACTGGCCAGGCTGCAAGCT 5120
 CAGAGGCCCTTGGACCAAGCTGGGTGGTGGCAACCAAGAGGATGTGGGTACCAACCTGAGCAGGTGGCACTCTCC 5200
 AAGTCTTAAGTACACACAGTGGAGATGCCAACTGCAGAAAGCTACAGGTAGGACACCTGAAGTGTCACTACAGAGCC 5280
 CTCUGAACACAGTTACACAGGGACAACCTCCAGAGCTGGTGGAGACACAGCTGAGAGGTGTCCACTCTGAGCCCTG 5360
 CGGTTCAATATCTAGCTCATTATGCTACAGAAAGTACTGCGAGGTAGGGGGGCCACCATGATGAGTTTATAGAGGTG 5440
 GGGCAATTGTACAGCTGTGAAGCTGAAAGAAATTGCTCAGGACCCAGATGTACTCAATCTTACCTTAGCTAGAGGTGG 5520
 TCCCTCAGAAATCTACACTGGTTTAAACCCCTTAAGTCCCTTAAATGGCAGAGATAGATCCAGAGTTCCAGGAACCC 5600
 AGGTCTCTCTCTAGCCAGGGGTAGAGAGCTTATTCTCTCTCTGAGAGAAAGTTGAGGAGCAGTGTGTGATCATTT 5680
 GGTGGTGGTCTCAGTCACTGTCTGACTCTTTGTGACCTCATGGACTATGGCCACCAGGCTCTCTGTCCATAGAAATCT 5760

Figure 2 (suite 1)

CCAGGCCAAGAACACTGGAGTGGGTGGCCATTTCCTTCTCCAGGGGATTTCCCTGCCAGGGATTAAACCCGAATTGGCA 5840
 GGTGGATTCTTTACCCGAGGCCACTAGAAAGTCCCATGTGATCATTAGATAATACTTATACCTCATTTCCTGATTAAAGTG 5920
 TAAACACAGAAATCTTCTGACACCACTTCCACCCCTGGATTCCCATCCCAAGTAGGTTTACCTGGAATTGTGTAGG 6000
 AATACTAAAAAGGAGAGTGAGATAGTGACACTATGACTTAACACATGTCMAATGCTGTGCCAGGACCTGGCACAGTG 6080
 TAGGGGTGATAAACATTTCGGGATGTCATAAATCTGACTCTAACCTCTGTGACTCTGGGSCAGTCATTTCCTCTGGGCT 6160
 TCTTTATCTTAAAAAATGAGAGTTTCAGCTCTGTGCTGATTCTAAGCCTGGATCCAGTAGCTCTGACTCTACCTGGAA 6240
 AAATGCTTGTGGGCTGTTTTCAGGTTAGTCATTTCCTTTTGGCTTTTAACTCTCTCTCCAGGCTCCCTG 6320
 AGTCCCTGCCCGATGACACTGCCACCTTAGTCTCTGAGAGGCCCAAGCCCCCTGGATTGTGTTCTGTATGCTATGG 6400
 CTCCTTTCCCTCACCCTGGACATTGCTCCGTGAGTCTTGCTACATTGTCCTGTAAGCTGGTGGAGGAGGCTGTGCTGC 6480
 TTAGGGTTGCCAGTGGAGACACACTTTGGAAGGAATTACTCACTGGACAAGGAGAATACCCAGATCCAGGGGTTTCA 6560
 TATGAAGGCAGAATGGGATTAGGGAGGACGCCGAGGACCTTCTGGCCATGGGCTTGGGGAGGATAGTAGAGGAGT 6640
 CTCAGACTTAAAAAATCTTGAACCTTTGACAGGGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTCATCCAGTGAAG 6720
 GAGATGCAATTTGAGCTGACTGTGCTTGGCAAGGCGGGTGAGTGTCCACGGTTGCCCTGAGAACTCCTGGGCTGACTGC 6800
 TGTCTGTCTCTGCTGTCTAGTGTCCCTTCCAGATTCCCTGAGCTAAGCTGACATCTCTCCAGGCTACCCAAAGGAAG 6880
 CCTGCATGGACATCTCATGCCCGCAGGTTGCTAGCTGCTGCCAGCGGCTGTGTCAGCCTGTGCCCCCGACGCCAGCTGC 6960
 CAGCTGGTTTTGCACCAGTACTGAAGGGTGGCTCAGGACCTACTGCTCAATGTGCTTTTGGCTGATGCCAATAGCCT 7040
 GGCATGCTCAGCACCCAGCTTGTGATGCTGCTAGGTAGTTGGACAGAGGTAGGATGAAGACAGGGGAGATGGTAGA 7120
 GGTTAACCTACTAGAGGAAGCAGACCTGAATGCAGCCGATATCTGGGATTCACCCATAGGGCAAGAGCAGGCTCAGGC 7200
 AGGCTCCTCTGTTGCTGGGCACTTGTGCTGCTAAGCCTTTGTTGCTGCTCTCTGATATACAGGTGAGATCCCCGC 7280
 CATCTGCTGCCACTCCTTATCCCTCTATTACCACCACCACCTTCTCATGGGAAGAAGAACCCACCAACCCCTTTGGG 7360
 AAAGTGTAGAGTCCAAAGAAAGAGCCAGACTTGGAGTTCAACAGGTCTAGGCTGCACTCTTGTGTTGGGACCTGGGG 7440
 AAGTCAATTAACCTCTTGAAGCACTGAAAAGTAGGAACATAATACCTGTCTGTGGGGCTGTTTTCAGGGCTCTAGAC 7520
 AATGTGAGTAAACACCTGGTTCTGAACAAAAGTGAATAAATGATGATCAATGACTGTTGTTATGAATAATATCAA 7600
 CAGTGGAGAAGAATCAGTGAATGAGTTCTCCACCTGCCAGAAAGGCAAAATCCCTAGGCTGGAGGGCTGAGGCTCTCA 7680
 AAGCAGGGAAGCTGTAGGCTGAGAGGGAATGCTCAGAGCTTACCATAAACAATAGAGAGGATTAACCTGTTGGTGAG 7760
 AAGAGGAGGAGGAGCAGGATCAAGACCAAGTCAACCTGGGTATGTTTATGCTTTTTTTTAGAGAAGCACAAAGAGGT 7840
 TGCATTGACCACCACCTAACCATATCCCTGCTTTTCTCCCAATATCAGGCGAAGACTTATGAAGCAAGGCTCAGCAGTC 7920
 CCCCTTCCCGACCTGCCACAGCTGAGAACCCAGTGGCTACGCTCTGCCCTGGGTCTTCCGCTCTTCCCCATTGCTGAGAG 8000
 CAAACCCCTCTCAGTGGACAGCAGGCTGAGTGCTCTTATGTGAAGTCATGATTACCCAGGTGGACAGCAGGCGCTGT 8080
 CTTTTCCTGCTCTCTCCCTCAGAGACTACCATTTGCTGCTGAATAAAGACTCAGAACTTG 8138

←TCTGCTGAAATAAAGACTCAGAACTTG **SIL9** (SEQ ID NO: 14)

Figure 2 (suite 2)

cDNA CH GGTCTTTGGTTGCTGGANGAAGACAGGATGGATCTGGTCTGAGAAATACCTTCTCC 60
cDNA RPE1 -----

cDNA CH ATGTGGCTCTGATGGGTGTTCTTCTGGCTGTAAGACCACAGAAGACCAGAGACAGGG 120
cDNA RPE1 -----

cDNA CH ACTGGCTTGGTGTCTCAAGGCAGCTCAGAATTAAGCATGGAACAGACAGCTGTATCCAG 180
cDNA RPE1 -----

cDNA CH AGTGGACAGAAAGCCAGGGCCCTGACTGCTGGAGAGGTGGCCACATATCCCTGAAGGTCA 240
cDNA RPE1 -----

cDNA CH GCAATGATGGGCCTACACTGATGGGGCAAATGCTTCTTCTCTATTGCCTTGCACTTTC 300
cDNA RPE1 -----

cDNA CH CTAAAAGCCAAAGGTGCTGCCAGATGGGCAGGTGCTCTGGGCCAACACACCATCATCA 360
cDNA RPE1 -----

cDNA CH ATGGGAGCCAGGTGTGGGAGGACAGCTGGTATATCCCAAGAACCTGATGATACCTGCA 420
cDNA RPE1 -----

cDNA CH TCTTCCCCGATGGGGAGCCCTGCCCTTCTGGCCCTCTATCTCAGAAAGATGCTTTGTTT 480
cDNA RPE1 -----

cDNA CH ATGCTCTGGAAGACCTGGGACCAATACTGGCAAGTTCGGGGGGCCCGTGTCTGGACTGA 540
cDNA RPE1 ----- CCAATACTGGCAAGTTCGGGGGGCCCGTGTCTGGACTGA 41

cDNA CH GCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTACTGTCTACCACC 600
cDNA RPE1 GCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTACTGTCTACCACC 101

cDNA CH GCCGGGGTCCCAGAGCTATGTGCCCTCGCTCACTCCAGTTCAGCCTTCACCATTAAGT 660
cDNA RPE1 GCCGGGGTCCCAGAGCTATGTGCCCTCGCTCACTCCAGTTCAGCCTTCACCATTAAGT 161

cDNA CH ACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGAGGCCTTGGATGGAAGGAACAAGC 720
cDNA RPE1 ACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGAGGCCTTGGATGGAAGGAACAAGC 221

cDNA CH GCTTCTGAGAAAGCAGCCTCTGACCTTTGCCCTCCAGCTCCATGATCCAGTGGCTATT 780
cDNA RPE1 GCTTCTGAGAAAGCAGCCTCTGACCTTTGCCCTCCAGCTCCATGATCCAGTGGCTATT 281

cDNA CH TGGCTGGGGCTGACCTTTCTACACCTGGGACTTTGGTGACAGTACAGGGACCTGATCT 840
cDNA RPE1 TGGCTGGGGCTGACCTTTCTACACCTGGGACTTTGGTGACAGTACAGGGACCTGATCT 341

cDNA CH CTCGGGCACTCAGGTCACACTTACCTAGAGTCTGGCCAGTCACTGCACAGGTGG 900
cDNA RPE1 CTCGGGCACTCAGGTCACACTTACCTAGAGTCTGGCCAGTCACTGCACAGGTGG 401

cDNA CH TGCTGACAGGCTGCCATTCCTCTCACCTCCTGTGGCTCCCTCCAGTTCACAGGCACTACAG 960
cDNA RPE1 TGCTGACAGGCTGCCATTCCTCTCACCTCCTGTGGCTCCCTCCAGTTCACAGGCACTACAG 461

Figure 3

| | | |
|-----------|---|------|
| cDNA CH | ATAGGCTATGTGACAACTGCAGAGGCTCTCTGGAACCAAGCTGGCCAAAGTGCTACTACAG | 1020 |
| cDNA RPE1 | ATAGGCTATGTGACAACTGCAGAGGCTCTCTGGAACCAAGCTGGCCAAAGTGCTACTACAG | 521 |
| ***** | | |
| cDNA CH | AAGTCATGGGCACCACCTGGCCAGGTGCCAACTGCAGAGGCCCTGGCACCACAGTTG | 1080 |
| cDNA RPE1 | AAGTCATGGGCACCACCTGGCCAGGTGCCAACTGCAGAGGCCCTGGCACCACAGTTG | 581 |
| ***** | | |
| cDNA CH | GGTGGGTGCCAACACAGAGGATGTAGTACCACTGAGCAGGTGGCAACCTCCAAAG | 1140 |
| cDNA RPE1 | GGTGGGTGCCAACACAGAGGATGTAGTACCACTGAGCAGGTGGCAACCTCCAAAG | 641 |
| ***** | | |
| cDNA CH | TCTTAAGTACAACACAGTGGAGATGCCAACTGCAAAAGCTACAGTAGGACCTGAAG | 1200 |
| cDNA RPE1 | TCTTAAGTACAACACAGTGGAGATGCCAACTGCAAAAGCTACAGTAGGACCTGAAG | 701 |
| ***** | | |
| cDNA CH | TGTCAACTACAGAGCCCTCTGGAACCAAGTTACACAGGGAACAACTCCAGAGCTGGTGG | 1260 |
| cDNA RPE1 | TGTCAACTACAGAGCCCTCTGGAACCAAGTTACACAGGGAACAACTCCAGAGCTGGTGG | 761 |
| ***** | | |
| cDNA CH | AGACCACAGCTGGAGAGGTGTCCACTCTGAGCCTGCGGGTTCAAATACTAGCTCATTC | 1320 |
| cDNA RPE1 | AGACCACAGCTGGAGAGGTGTCCACTCTGAGCCTGCGGGTTCAAATACTAGCTCATTC | 821 |
| ***** | | |
| cDNA CH | TGCCTACAGAAGGTACTGCAGGCTCCCTGAGTCCCTGCCGATGACACTGCCACCTTAG | 1380 |
| cDNA RPE1 | TGCCTACAGAAGGTACTGCAGGCTCCCTGAGTCCCTGCCGATGACACTGCCACCTTAG | 881 |
| ***** | | |
| cDNA CH | TCCTGGAGAAGCGCCAAAGCCCCCTGGATTGTGTTCTGTATCGCTATGGCTCCTTTTCC | 1440 |
| cDNA RPE1 | TCCTGGAGAAGCGCCAAAGCCCCCTGGATTGTGTTCTGTATCGCTATGGCTCCTTTTCC | 941 |
| ***** | | |
| cDNA CH | TCACCTGGACATTGTCCAGGATTGAGAGTGCTGAGATCCTACAGGCTGTGTATCCA | 1500 |
| cDNA RPE1 | TCACCTGGACATTGTCT---AGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTATCCA | 998 |
| ***** | | |
| cDNA CH | GTGAAGGAGATGCATTGAGCTGACTGTCTTGCCAAGGCGGGCTACCCAAGGAAGCCT | 1560 |
| cDNA RPE1 | GTGAAGGAGATGCATTGAGCTGACTGTCTTGCCAAGGCGGGCTACCCAAGGAAGCCT | 1058 |
| ***** | | |
| cDNA CH | GCAATGGACATCTCATCGCCAGGTTGTCAGCTGCCTGCCAGCGGCTGTGTACGCTGTGC | 1620 |
| cDNA RPE1 | GCAATGGACATCTCATCGCCAGGTTGTCAGCTGCCTGCCAGCGGCTGTGTACGCTGTGC | 1118 |
| ***** | | |
| cDNA CH | CCCCCAGCCAGCCTGCCAGCTGGTTTTGCAACAGGTACTGAAGGTTGGCTCAGGACCT | 1680 |
| cDNA RPE1 | CCCCCAGCCAGCCTGCCAGCTGGTTTTGCAACAGGTACTGAAGGTTGGCTCAGGACCT | 1178 |
| ***** | | |
| cDNA CH | ACTGCCTCAATGTGCTTTGGCTGATGCCAATAGCCTGGCGATGGTCAGCACCCAGCTTG | 1740 |
| cDNA RPE1 | ACTGCCTCAATGTGCTTTGGCTGATGCCAATAGCCTGGCGATGGTCAGCACCCAGCTTG | 1238 |
| ***** | | |
| cDNA CH | TCATGCTGGGCAAGAAGCAGGCTCAGGAGGCTCCTCTGTTCTGGGGATCTTGCTGG | 1800 |
| cDNA RPE1 | TCATGCTGGGCAAGAAGCAGGCTCAGGAGGCTCCTCTGTTCTGGGGATCTTGCTGG | 1298 |
| ***** | | |
| cDNA CH | TGCTAACAGCTTTGTTGCTTGATCTCTGATATACAGGCGAAGACTTATGAAGCAAGCT | 1860 |
| cDNA RPE1 | TGCTAACAGCTTTGTTGCTTGATCTCTGATATACAGGCGAAGACTTATGAAGCAAGCT | 1358 |
| ***** | | |
| cDNA CH | CAGCAGTCCCCCTTCCCAGCTGCCACAGGTAGAACCAGTGGCTACGCTGCCCTGGG | 1920 |
| cDNA RPE1 | CAGCAGTCCCCCTTCCCAGCTGCCACAGGTAGAACCAGTGGCTACGCTGCCCTGGG | 1418 |
| ***** | | |

Figure 3 (suite 1)

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cDNA CH      TCTTCGGCTCTTGCCCCATTGGTGAGAGCAAACCCCTCCTCAGTGGACAGCAGGTCTGAG 1980
cDNA RPE1    TCTTCGGCTCTTGCCCCATTGGTGAGAGCAAACCCCTCCTCAGTGGACAGCAGGTCTGAG 1478
*****

cDNA CH      TGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGTCTTTTCTCTGGT 2040
cDNA RPE1    TGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGTCTTTTCTCTGGT 1538
*****

cDNA CH      CTTCCCTCAGAGACTACCATTCGCTGAAATAAAGACTCAGAACTTG 2086 (SEQ ID NO: 15)
cDNA RPE1    CTTCCCTCAGAGACTACCATTCGCTGAAATAAAGACTCAGAACTTG 1584 (SEQ ID NO: 16)
*****

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Figure 3 (suite 2)


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Prot. CH      MDLVLRKYLHLHVALMGVLLAVRTTEGPRDRDWLGVSRLRIKAWNRLYPETWESQGFDC 60
Prot. RPE1    -----

Prot. CH      WRGGHISLKVSNDGPTLIGANASFSLAHFPKSKQVLDPGQVIWANNTIINGSQVWGQQL 120
Prot. RPE1    -----

Prot. CH      VYFQEPDDTCIFPDGECPCSGPLSQKRCFVYVWKTDWQYVQVLGGFPVSGLSIGTDKAMLG 180
Prot. RPE1    -----QYVQVLGGFPVSGLSIGTDKAMLG 23
                  *****

Prot. CH      TYNMEVTVYHRRGSQSYVPLAHSSSAFTITDQVPFSVSVSOLQALDGRNKRFLRKQPLTF 240
Prot. RPE1    TYNMEVTVYHRRGSQSYVPLAHSSSAFTITDQVPFSVSVSOLQALDGRNKRFLRKQPLTF 83
                  *****

Prot. CH      ALQLHDPSCGYLAGADLSYTWDFGDSTGTLLISRALTVHTHTYLESGPVTAQVVLQAAIPLTS 300
Prot. RPE1    ALQLHDPSCGYLAGADLSYTWDFGDSTGTLLISRALTVHTHTYLESGPVTAQVVLQAAIPLTS 143
                  *****

Prot. CH      CGSSPVPGTDDRHVITAEAPGTTAGQVPTTEVMGTTTPGQVPTAEAPGTTVGWVPTTEDVG 360
Prot. RPE1    CGSSPVPGTDDRHVITAEAPGTTAGQVPTTEVMGTTTPGQVPTAEAPGTTVGWVPTTEDVG 203
                  *****

Prot. CH      TTPEQVATSKVLSTTPVEMPTAKATGRTPEVSTTEPSGTTVTQGITPELVETTAGEVSTP 420
Prot. RPE1    TTPEQVATSKVLSTTPVEMPTAKATGRTPEVSTTEPSGTTVTQGITPELVETTAGEVSTP 263
                  *****

Prot. CH      EPAGSNTSSEMPTETAGSLSPDPDTATLVLEKRAQLDCVLYRYGSFSLTLDIVQGE 480
Prot. RPE1    EPAGSNTSSEMPTETAGSLSPDPDTATLVLEKRAQLDCVLYRYGSFSLTLDIV-SIE 322
                  *****

Prot. CH      SAEILQAVSSSEGDFAELTVSCQGGPKKEACMDISSPGCQLPAQRLCQVPVPPSPACQLVL 540
Prot. RPE1    SAEILQAVSSSEGDFAELTVSCQGGPKKEACMDISSPGCQLPAQRLCQVPVPPSPACQLVL 382
                  *****

Prot. CH      HQVLKGGSGTYCLNVSLADANSLAMVSTQLVMPGQEAGLRQAPLFVGILLVLTALLASI 600
Prot. RPE1    HQVLKGGSGTYCLNVSLADANSLAMVSTQLVMPGQEAGLRQAPLFVGILLVLTALLASI 442
                  *****

Prot. CH      IYRRRLMKQGSAPVLPQLPHGRTQWLRLPWVFRSCPIGESKPILLSGQQV 649 (SEQ ID NO: 17)
Prot. RPE1    IYRRRLMKQGSAPVLPQLPHGRTQWLRLPWVFRSCPIGESKPILLSGQQV 491 (SEQ ID NO: 18)
                  *****

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Figure 4